

U.S.S.N. 09/663,968

Yip

AMENDMENT

removing the residual baseline from the intermediate data set to generate a corrected data set;  
locating a probable peak in the corrected data set; and  
identifying, using the located probable peak, the biological sample.

38. (3x Amended) A system for identifying a biological sample, the system comprising:

an instrument receiving the biological sample and generating a data set comprising data of the components in the biological sample;

a computer communicating to the instrument and configured to receive the generated data set, the computer performing the method of:

denoising the data set to generate denoised data;

correcting the baseline from the denoised data to generate an intermediate data set;

defining putative peaks for the biological sample;

using the putative peaks to remove residual baseline effects, generating a residual baseline;

removing the residual baseline from the intermediate data set to generate a corrected data set;

locating a probable peak in the corrected data set; and

identifying, using the located probable peak, the biological sample.

40. (2x Amended) A machine readable program operating on a computing device, the computing device being configured to receive a data set comprising data of the components in a biological sample, wherein the program implements the steps of:

denoising the data set to generate denoised data;

intermediate data set;

defining putative peaks for the biological sample;

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using the putative peaks to remove residual baseline effects,  
generating a residual baseline;  
removing the residual baseline from the intermediate data set to  
generate a corrected data set;  
locating a probable peak in the corrected data set; and  
identifying, using the located probable peak, the biological sample.

41. (2x Amended) A system for identifying a component of a DNA sample, comprising:

a mass spectrometer receiving the DNA sample and generating a data set comprising data of the components in the DNA sample;

a computing device configured to receive the data set, the computing device implementing the method comprising:

denoising the data set to generate denoised data;  
correcting the baseline from the denoised data to generate a corrected data set, the corrected data set having putative peaks;  
using the putative peaks to remove residual baseline effects;  
locating a probable peak in the corrected data set; and  
identifying, using the located probable peak, a component in the composition of the DNA sample.

45. (2x Amended) A system for identifying a component in a biological sample, comprising:

an instrument receiving the biological sample and generating a data set comprising data of the components in the biological sample;

a computing device receiving the data set and performing the steps of:  
generating corrected data by processing the data set to remove

using the putative peaks to remove residual baseline effects;

using the putative peaks to remove residual baseline effects;